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☐ 1: [P54725](#). UV excision repai...[gi:1709983]

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LOCUS P54725 363 aa linear PRI 15-SEP-2003
 DEFINITION UV excision repair protein RAD23 homolog A (HHR23A).
 ACCESSION P54725
 VERSION P54725 GI:1709983
 DBSOURCE swissprot: locus R23A_HUMAN, accession P54725;
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: Sep 15, 2003.
 xrefs: gi: 498145, gi: 498146, gi: 1905905, gi: 1905912, gi: 23664449, gi: 23664450, gi: 33878469, gi: 15559329, gi: 1082759, pdb accession 1DV0, pdb accession 1F4I, pdb accession 1IFY
 xrefs (non-sequence databases): GenewHGNC:9812, MIM 600061, GOGO:0003697, GOGO:0006289, InterProIPR004806, InterProIPR006636, InterProIPR000449, InterProIPR000626, PfamPF00627, PfamPF00240, SMARTSM00727, SMARTSM00165, SMARTSM00213, TIGRFAMsTIGR00601, PROSITEPS50030, PROSITEPS50053
 KEYWORDS DNA damage; DNA repair; Nuclear protein; 3D-structure; Repeat; Polymorphism.
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 363)
 AUTHORS Masutani,C., Sugasawa,K., Yanagisawa,J., Sonoyama,T., Ui,M., Enomoto,T., Takio,K., Tanaka,K., van der Spek,P.J., Bootsma,D., Hoeijmakers,J.H.J. and Hanaoka,F.
 TITLE Purification and cloning of a nucleotide excision repair complex involving the xeroderma pigmentosum group C protein and a human homologue of yeast RAD23
 JOURNAL EMBO J. 13 (8), 1831-1843 (1994)
 MEDLINE 94222030
 PUBMED 8168482
 REMARK SEQUENCE FROM N.A.
 REFERENCE 2 (residues 1 to 363)
 AUTHORS Lamerdin,J.E., McCready,P.M., Stilwagen,S., Ramirez,M. and Carrano,A.
 TITLE Direct Submission
 JOURNAL Submitted (~MAR-1997)
 REMARK SEQUENCE FROM N.A.
 REFERENCE 3 (residues 1 to 363)
 AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A., Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
 TITLE Direct Submission
 JOURNAL Submitted (~OCT-2002)

REMARK SEQUENCE FROM N.A., AND VARIANTS ALA-131 AND MET-200.
REFERENCE 4 (residues 1 to 363)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REMARK SEQUENCE FROM N.A.
TISSUE=Pancreas
REFERENCE 5 (residues 1 to 363)
AUTHORS Dieckmann,T., Withers-Ward,E.S., Jarosinski,M.A., Liu,C.F.,
Chen,I.S. and Feigon,J.
TITLE Structure of a human DNA repair protein UBA domain that interacts
with HIV-1 Vpr
JOURNAL Nat. Struct. Biol. 5 (12), 1042-1047 (1998)
MEDLINE 99061330
PUBMED 9846873
REMARK STRUCTURE BY NMR OF 319-363.
REFERENCE 6 (residues 1 to 363)
AUTHORS Withers-Ward,E.S., Mueller,T.D., Chen,I.S. and Feigon,J.
TITLE Biochemical and structural analysis of the interaction between the
UBA(2) domain of the DNA repair protein HHR23A and HIV-1 Vpr
JOURNAL Biochemistry 39 (46), 14103-14112 (2000)
MEDLINE 20541363
PUBMED 11087358
REMARK STRUCTURE BY NMR OF 319-363.
COMMENT -----
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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] Involved in postreplication repair of UV-damaged DNA.
Postreplication repair functions in gap-filling of a daughter
strand on replication of damaged DNA (Potential).
[SUBUNIT] Interacts with MJD.
[SUBCELLULAR LOCATION] Nuclear (Probable).
[DOMAIN] The ubiquitin-like domain mediates interaction with MJD.
[SIMILARITY] Contains 1 ubiquitin-like domain.
[SIMILARITY] Contains 2 UBA domains.
FEATURES Location/Qualifiers

source 1..363
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..363
/gene="RAD23A"
Protein 1..363
/gene="RAD23A"
/product="UV excision repair protein RAD23 homolog A"
Region 1..81
/gene="RAD23A"
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Region 131
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/note="T -> A. /FTid=VAR_016251."
Region 161..201
/gene="RAD23A"
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/note="UBA 1."
Region 200
/gene="RAD23A"
/region_name="Variant"
/note="T -> M. /FTid=VAR_016252."
Region 318..358
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/region_name="Domain"
/note="UBA 2."
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/gene="RAD23A"
/region_name="Helical region"
Region 325..331
/gene="RAD23A"
/region_name="Hydrogen bonded turn"
Region 334..341
/gene="RAD23A"
/region_name="Helical region"
Region 342..345
/gene="RAD23A"
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Region 348..354
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Region 355..356
/gene="RAD23A"
/region_name="Hydrogen bonded turn"

ORIGIN

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241 fqnmrqviqq npallpallq qlgqenpql qqisrhqeqf iqmlneppge ladisdvege
301 vgaigeeapq mnyiqvtpqe keaierlkal gfpeslviqa yfaceknenl aanflsqnf
361 dde
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